

hApo2LI 31 D C A G D F H K K I G L F C C R G C P A G H Y L K A P C T E P C S N S T C L
hTNFR1 43 V C P O G K . . . Y I M P O N N S I C C T K C H K G T V L Y N D C P G P G O D T D C R
hTNFR2 35 T C R L R E . . . Y Y D O T A O M C C S K C S P G O H A K V F C T K T . S O I V C D
hTNFRcp 42 T C R D O E K E . Y Y E P O H R I C C S R C P P G T Y V S A K C S R I . R D T V C A
hFAS/Apo1 48 N L E G L H H O G O F C H K P C P P G E R K A R D C T V N G D E P D C V
hLNGFR 31 A C P T G L Y T H S G E C C K A C N L G E G V A O P C G A . . N O T V C E
hCD40 25 A C R E K O Y L I N S O C C S L C O P G O K L V S D C T E F . T E T E C L
hCD27 26 S C P E R H Y W A O G K L C C O M C E P G T F L V K D C O H R K A A O C D
hCD30 28 T C H G N P S H . Y Y D K A V R R C C Y R C F M G L F P T O O C P O R . . P T D C R K
hOX40 30 H C V G D T Y P S N O R C C H E C R P G N G M V S R C S R S . O N T V C R

hApo2LI 72 V C P O D . T F L A W E N H H S E C A R C . O A C D E O A S O V A L E N C S A V A D T R C G
hTNFR1 83 E C E S G . S F T A S E N H L R H C L S C . S K C R K E M G O V E I S S C T V D R D T V C G
hTNFR2 77 S C E D S T Y T O L W N W V . P E C L S C G S R C S S . . D O V E T O A C T R E O N R I C T
hTNFRcp 82 T C A E N S Y N E H W N Y L . T I C O L C . R P C D P V M G L E E I A P C T S K R K T O C R
hFAS/Apo1 84 P C Q E G K E Y T D K A H F S S K C R R C . R L C D E G H G L E V E I N C T R T O N T K C R
hLNGFR 66 P C L D S V T F S D V S A T E P C K P C . T E C V G L . . O S M S A P C V E A D D A V C R
hCD40 61 P C G E S E F L D T W N R E . T H C H O H . K Y C D P N L G L R V O O K G T S E T O T I C T
hCD27 64 P C I P G V S F S P D H H T R P H C E S C . R H C N S G L L V R . . N C T I T A N A E C A
hCD30 68 O C E P D . Y Y L D E A D R . . C T A C . V T C S R D D L V E K T . P C A W N S S R V C E
hOX40 66 P C G P G . F Y N D V V S S K P . C K P C . T W C N L R S G S E R K O L C T A T O D T V C R

hApo2LI 116 C K P G W F Y E C O V S O C V S S S P F Y C O P C L O C G A L H R H R T R L L C S R R D . T D C G . T
hTNFR1 127 C R K N O Y R H Y W S E N L F O C F N C S L C L N G . . T V H L S C O E K O N T V C . . T
hTNFR2 120 C R P G W Y C A L S K O E G C R L C A P L R K C R P G . F G V A R P G T E T S D V V C K . P
hTNFRcp 126 C O P G M F C A A W A L E C T H C E L L S D C P P G T E A E L K D E V G K G N H C V . F
hFAS/Apo1 124 C K P N F F . . C N S T V C E H C D F G T K C E H G I . . . I K E C T L T S N T K C K .
hLNGFR 109 C A Y G Y Y O D E T T G R C E A C R V C E A G S G L . V F S C O D K O N T V C I E . E
hCD40 105 C F E G W H C I S E A C E S C V L H R S C S P G F G . V K O I A T G V S D T I C E P
hCD27 106 C R N G W O C R D K E C T E C D P L P N P S L T A R S S O A L S P H P O P T H L P .
hCD30 108 . C R P G M F C S T S A V N S C A R C F F H S V C P A G M I V K F P G T A O K . N T V C E .
hOX40 109 . C R A G T O P L D S Y K P G V D C A

hApo2LI 164 C L P G F Y E H G D G C V S C P T
hTNFR1 168 G H A G F F L R E N E C V S C S N C K K S L E C T K L C L
hTNFR2 164 G A P G T F S N T T S S T D I C R P H O I C N V V A I P G N A S M D A V C T
hTNFRcp 170 C K A G H F O N T S S P S A R C O P H T R C E N O G L V E A A P G T A Q S D T T C K
hLNGFR 149 C P D G T Y S D E A N H V D P C L P C T V C E D T E R Q L R E C T R W . A D A E C E
hCD40 145 C P V G F F S N V S S A F E K C H P W T S C E T K D L V V O O A G T N K T D V V C G
hOX40 127 P C P P G H F S P G D . . H O A C K P W T H C T L A G K H T L O P A S N S S D A I C E

Fig. 2

09634-11301

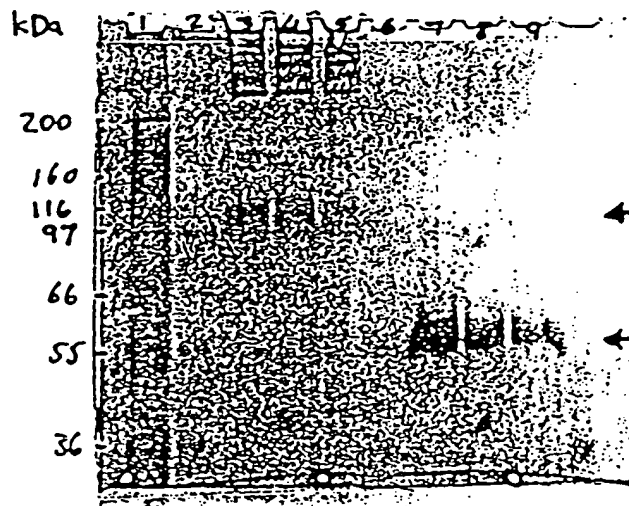


Fig. 3

SECRET

1	CGCGCCGTCG	GGCGCGCGCG	CTGAGCGCG	AGCCAGCG	GGCAGAGCG	AGCGAGCGCG
61	GAAGCGCGTC	GGCGCGCGTC	CGAGCGCTAT	CGAGAGCGCG	CGCGCGCGCT	CGCGCGCGCT
1			M	E	O	R
121	GGCGCGCGCG	CTGCTGCTCG	TGCTGCTGCG	GGCGCGCGCG	CAGCGCGCG	CTGCTGCGCG
12	A	A	L	L	V	L
181	CAGCTGTGAC	TGTCGCGCTG	ACTGTGCAAA	GAGATCTGCT	CTGTCTTGTG	CGACGAGCG
32	R	C	D	C	A	G
241	CGCAGCGCGG	CAGTACCTGA	AGCGCGCTTG	CAGCAGCGCG	TGCGCGAAGT	CGACCTGCGT
52	P	A	G	H	I	L
301	TGCTGTGCGC	CGACGACACT	TGCTGCGCTG	CGACAGCGAC	CATATATGCG	AAATGTGCGCG
72	V	C	P	Q	D	T
361	CTGCGAGCGC	TGCTATGAGC	AGCGCTGCGA	GCTGCGCGCG	GAGAGCTGTT	CAGCACTGCG
92	C	Q	A	C	D	E
421	CGACGAGCGC	TGTCGCTGTA	AGCGCGCTG	CTTGTGCGAG	TGCGCGCTG	CGCTATGCG
112	D	T	R	C	G	K
481	CAGCAGCTCA	CGCTTCTACT	CGCAACCTAG	CGTACAGTGC	GGCGCGCTGC	ACGCGCAGC
132	S	B	S	P	F	Y
541	AGCGCTACTG	TGTTGCGCGA	GAGATACCTA	CTGTGCGAGC	TGCGCTGCGCG	CGTTCTATGA
152	R	L	L	C	S	R
601	ACATGCGCAT	GGCTGCGCTG	CTGTGCGCGA	GAGCAGCGCG	GGAGCGCTGC	CAGAGCGCG
172	H	G	D	G	C	V
661	TGCGCTGTG	TGTCGCGTGA	CGCAGATGTT	CTGCGCTGCG	GTCGCGCTG	CTGCGCTGCT
192	A	A	V	C	G	W
721	GGTGCCTGTC	CTGCTGCGCG	CGACCTGTAC	CTACAGATAC	CGCGCTGCTG	GGCTGCGA
212	V	P	L	L	L	G
781	CGCGCTGCTT	ACTGCGATGC	AAAGCTGCGT	GGAGCTGCTG	AGCCGACGAC	CGCGCGCGCG
232	P	L	V	T	A	D
841	TGCTGCGCGC	TGCGAGCGCG	CGCAGACCGT	TCTAGCAGCT	CTGTAGCAGCA	GTCAGAGAT
252	L	S	P	L	D	S
901	CTGCGCGCGC	CAGTGTGCTG	CTAACAGTGC	GACCGCTGCG	TACCCGCGA	CCGCGAGCG
272	C	T	V	Q	L	V
961	CGTGTGCGCG	CAGCTGACAT	GCTGCTGCGA	CGAGTGTGCG	AGCAGAGCTG	TGCGCGCGCG
292	L	C	P	Q	V	T
1021	TGCTGCGCGC	ACATGTGCGC	CAGAGTGTGCG	AGCGCGCTGC	CGAGCGCGTA	TGCTGCGAGCG
312	A	A	P	T	L	S
1081	GGCGCGCAG	CTGTACAGCG	TGATGAGCGC	GCTGCGCGCG	CGCGCTGCGA	AGGAGTGTCT
332	G	P	Q	L	Y	D
1141	CGACCTGCTG	GGCGCTGCGC	AGCGAGAT	CGAGCGCTGC	GAGTGTGCGA	TGCGCGCTG
352	R	T	L	G	L	R
1201	CGCAGACGAG	CAGTACAGCA	TGCTGAGCGC	CTGCGCGCGC	CAGCAGCGCG	CGCGCTGCGG
372	R	D	Q	Q	Y	E
1261	AGCGCTGTAC	GGCGCGCTGC	AGCGAGTGC	GCTGCGCGCG	TGCGCTGTGAG	ACTGTGCGAG
392	A	V	Y	A	A	L
1321	CGCGCTGCGA	CGCGCGCGCT	GACAGCGCGC	CGACTTGCGA	CGTAGCGCGT	CTGTGTGCGCG
412	R	L	Q	R	G	B
1381	TGCGAGAGCG	CGTACGACCG	GTTACTGTATG	CGCTGACAGA	TGTTATGTGA	CTTATTGAGC
1441	CGCTGCGACG	CGCGTGTGTA	CGACGACGAC	CGCGCGCGCG	CGCTGCTGCG	CGCTATGCGT
1501	CGCGCGCGCG	CGAGAGCGA	CGAGCGAGTG	TGCGAGCGCG	CTGAGAGCAT	TGCTCACTT
1561	CTGCGCGCGA	GTTTGTGCTGA	GATGCGCGTA	TGTAATCTGT	GAGAGAGAG	AAAAAAGAAA
1621	AAAAAAGAAA	AAAA				

Fig. 4

Apoc3	1	MEORPRGCAAVAAALLLVLLCARAOCCTRSPR--	
TNFR1	1	MCLSTVPLDLEPL-VLLELLVGIYPSGVCICLVPHCDREKRSVY	
Fas/Apo1	1	MLGIMTLLPLVLTSTVARELSSKSVNAQVADINDSKCLERKTVTV	
Apoc3	33	CDACGDFHHKKKICLFCCRCPCAGHYLKAFCCTEPCCGNSTCLV	
TNFR1	44	CPQGGKIHPONNSICCTKCHKCTYLYNDPCGPGQDQTCRE	
Fas/Apo1	45	ETQNLGLHHDCQFCCHKPCPPERKARDCATVNCDEPDCVP	
Apoc3	73	CPQDFTFLAWENHHNSFCARCAQACDEQAASQVALENCSAVADTRCG	
TNFR1	85	CESGSFTASENHLRH-CLSSCKRKMCGVEISSCTVDTRTVCC	
Fas/Apo1	85	COEGKEYTDKAHFSSKCRRCRLCDECHGLEVEINCTRTQNTKCR	
Apoc3	117	CKPCGWFVEQVVSQCVQVSSSPFYCPQPCLDCCALHRRHTLLCSRRD-F	
TNFR1	127	CRKNQYRHYNSENLFQ----CFNCSCLNGCTVHLS--COEQNTQ	
Fas/Apo1	129	CKNPF-CNSITVCEH----CDPCTKCEHGIIKE--CTLTEN	
Apoc3	165	CLPGFYEHGDCQVSCPTSTLTGSCP--ERCAAVCGM	
TNFR1	168	CHAGFLRENECQVSCS-----NCKKSLECTKLCLP	
Apoc3	338	VMDAVPARWKNFVRVTLCLREARETEAVEVEICR--FEDQYTE	
TNFR1	333	VVENVPLRWKFFVRLTCLREARETEAVEVEICR--FEDQYTE	
Fas/Apo1	220	IAGVMTLSQVKEVERKNGVSEHKEIDRELCNCE--CLREAQYS	
FADD	104	ICDNYCK-DNRRLARQLKVSQDKIDSLIEDRYPN-ITERVRE	
TRADD	211	NEPLSK-DQQTARSVGLKWKVGR-SLCTGCRALHEDFPALD	
RIP	291	IRENLCK-HAKNKACNLGFTOSALIDEIDHDYFDCGKFKVQ	
Reader	1	MAVAFYIPDQATLLREAEQKQQLRLRESGWE	
Apoc3	378	MLKKEWRQOQP--AGLGAVYAALERMCL-DGCVFEDLRS	
TNFR1	374	MLATWRERTPRERATLELTCRVLRDMDL-LCEEDIEE	
Fas/Apo1	261	LRNWHQLHC-KKEAYDTLIKLLKKNCTLA-EKQTV	
FADD	144	SLERIMKNTK-CKEATVAHLVGLRSC--QMRVADLV	
TRADD	51	SLAYETREGLYEQAFQLRRFV-QAEGRRATQRLVE	
RIP	332	MLQKVMVREGIKCATVCKLQAQALHQC--SRIDPLSLT	
Reader	34	FLATVVLTKQYTSCHPTCKSKSKYKP	

Fig. 6

378	MLK	WR	Q	Q	P	--	--	A	G	L	G	A	V	A	A	L	E	R	M	C	L	--	D	G	C	V	E	D	L	R
379	MLA	WR	E	R	T																									

1621 AAAAAAAAAA AAAA

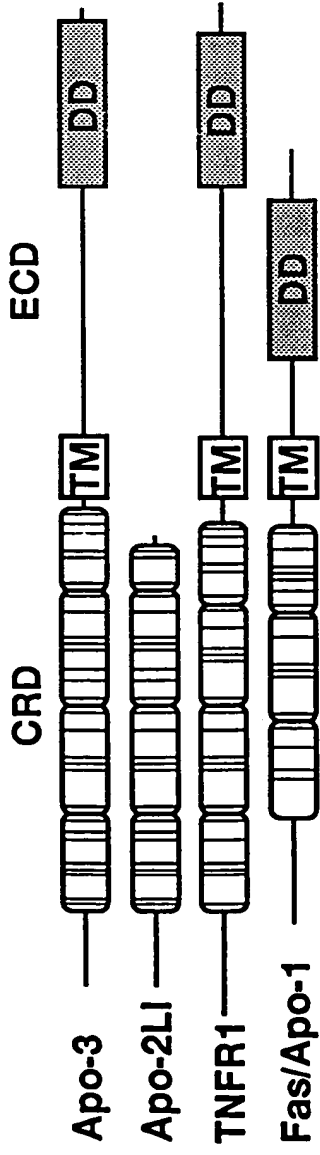


Fig. 7

FOOT - 1000000

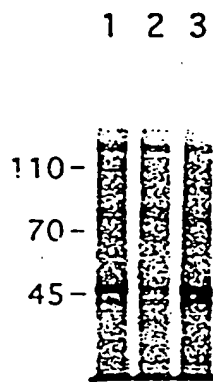


Fig. 8

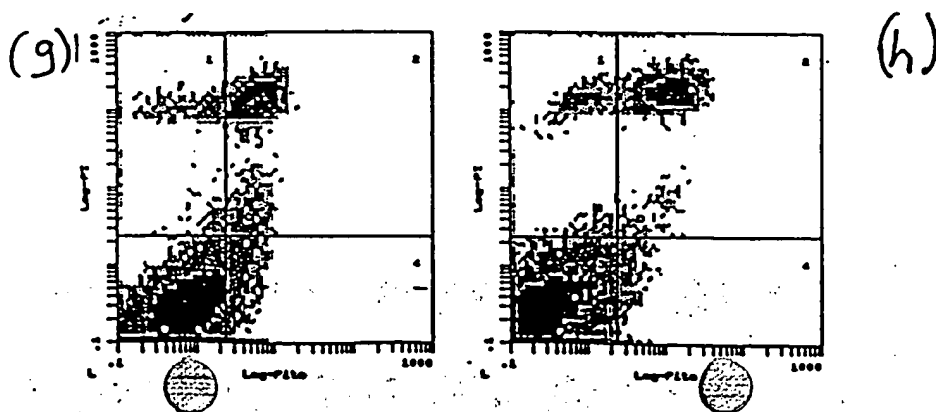
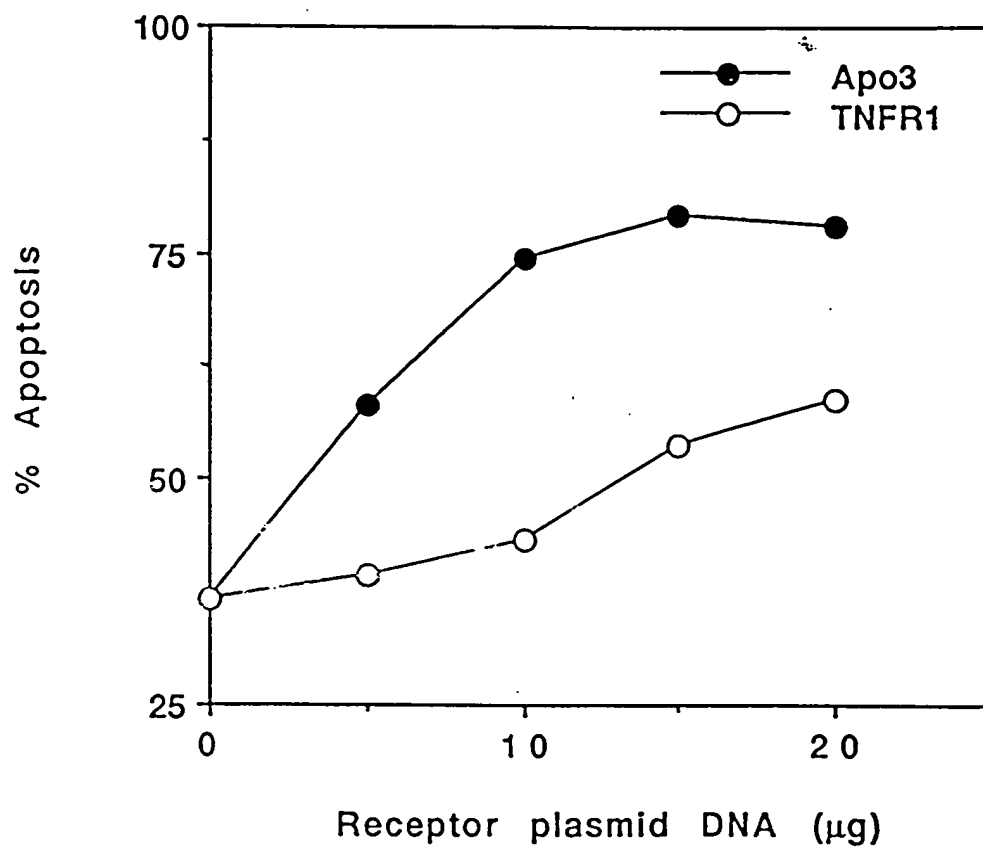


Fig. 9i



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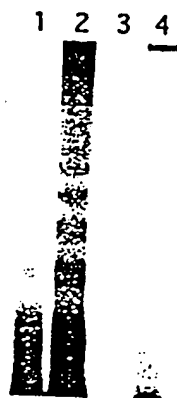


Fig. 9j

1 2 3 4 5 6 7 8 9

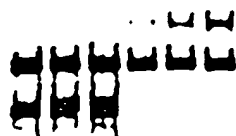


Fig. 10

TOGETHER "HE2E660

Transfection

pRK5

TNFR1

Apo-3



◀ Phospho-C-Jun

Fig. 11

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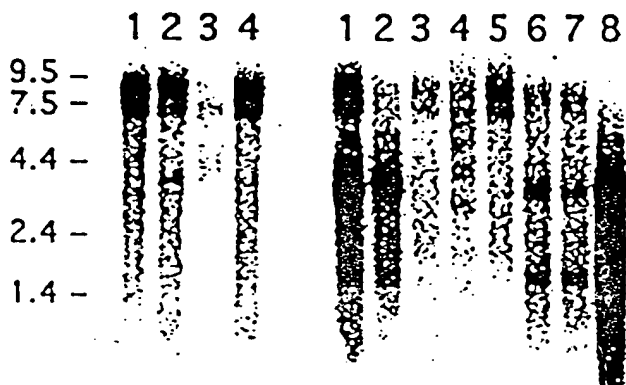


Fig. 12